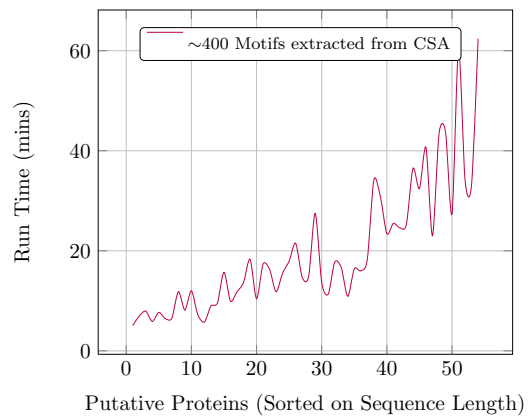


(a)



(b)

Supplementary Fig. 8: **(a)**: Runtimes for running CLASP. The runtimes have been divided into the three most time intensive parts - the 3D matching, running PDB2PQR which assigns charges on the proteins and APBS which calculates the potential. **(b)**: Runtimes when each of ~ 50 putative proteins was run on ~ 400 motifs that were automatically extracted from the CSA Database.